



MEME

Multiple Em for Motif Elicitation

For further information on how to interpret these results or to get a copy of the MEME software please access <http://meme-suite.org>.

If you use MEME in your research, please cite the following paper:

Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology*, pp. 28-36, AAAI Press, Menlo Park, California, 1994. [[pdf](#)]

[DISCOVERED MOTIFS](#) | [MOTIF LOCATIONS](#) | [INPUTS & SETTINGS](#) | [PROGRAM INFORMATION](#)

DISCOVERED MOTIFS

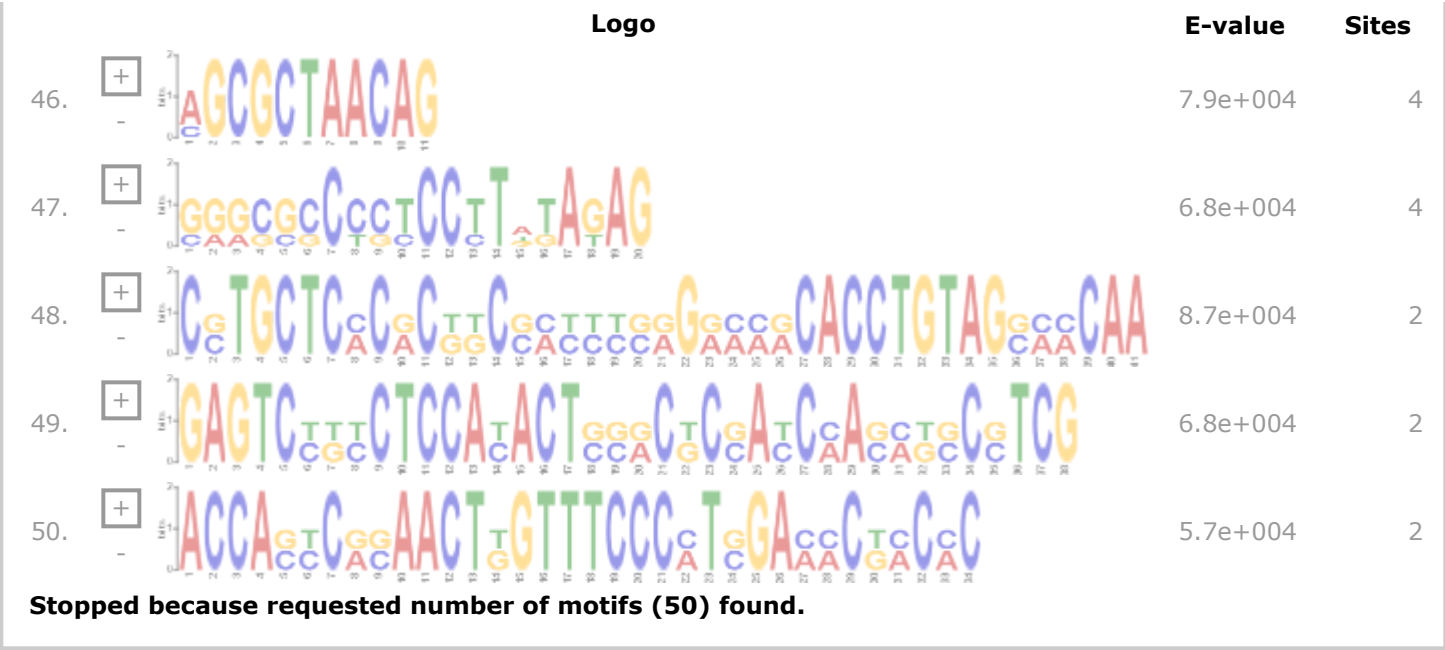
	Logo	E-value	Sites
1.		4.3e-152	329
2.		7.8e-112	95
3.		1.5e-045	36
4.		3.1e-035	17
5.		7.5e-034	5
6.		2.9e-023	12
7.		5.9e-014	12
8.		2.4e-007	20
9.		1.7e-006	12
10.		4.4e-006	6
11.		5.4e-005	18

Stopped because requested number of motifs (50) found.

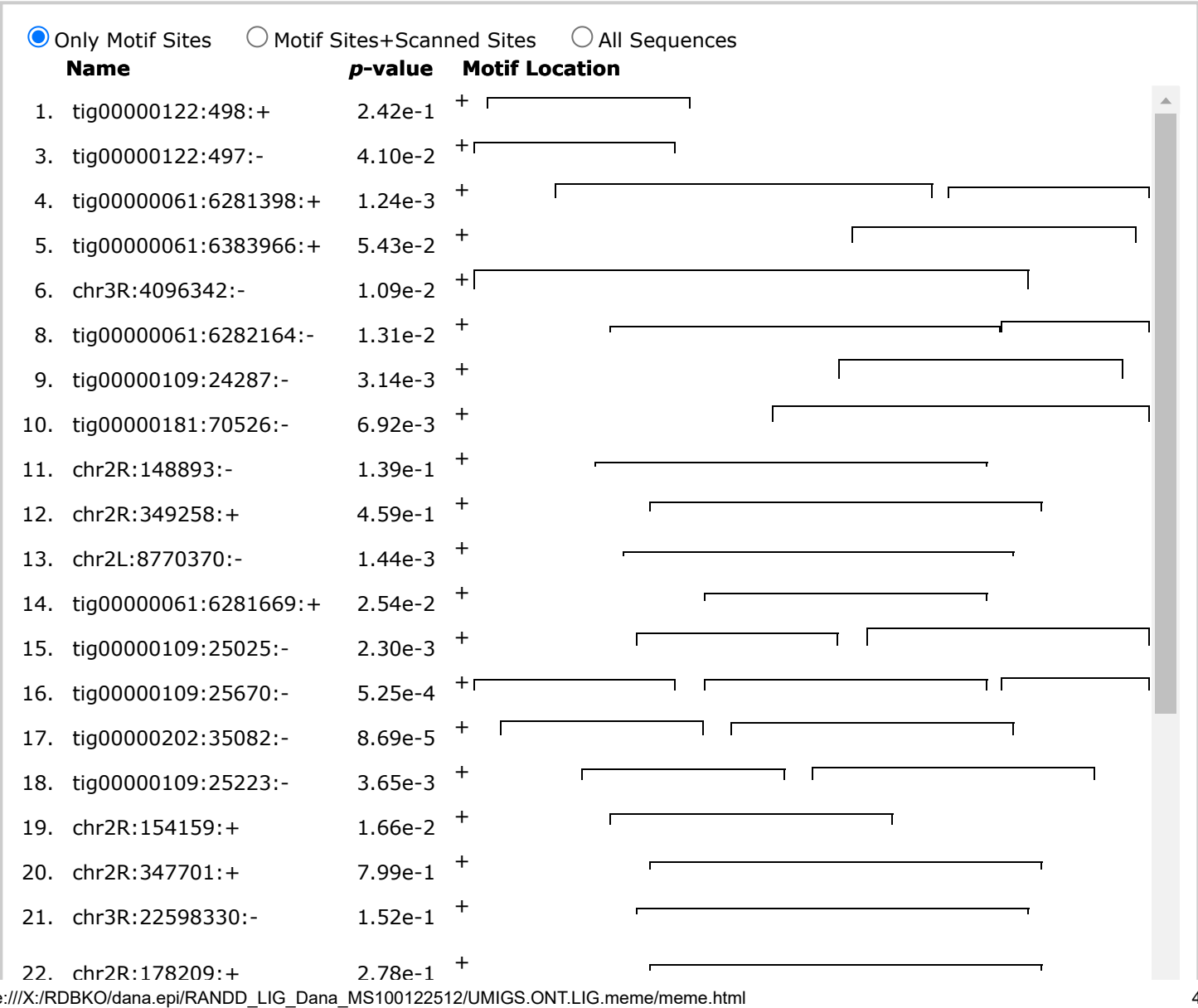
	Logo	E-value	Sites
12.		1.6e-003	8
13.		2.6e-003	4
14.		1.2e-002	9
15.		1.7e-002	6
16.		8.7e-002	6
17.		1.9e+000	4
18.		1.7e+001	10
19.		2.1e+001	4
20.		1.3e+002	4
21.		1.7e+002	7
22.		2.9e+002	4
23.		6.3e+002	4
24.		7.7e+002	7
25.		1.0e+003	6
26.		1.4e+003	2
27.		2.1e+003	10
28.		2.7e+003	4

Stopped because requested number of motifs (50) found.

Stopped because requested number of motifs (50) found.



MOTIF LOCATIONS



2/22/2021

MEME

24.	tig00000073:359558:+	5.16e-5	+	
25.	tig00000061:6281640:+	3.96e-1	+	
26.	tig00000202:34550:-	8.43e-2	+	
			+	

INPUTS & SETTINGS

Sequences

Source	Alphabet	Sequence Count
UMIGS.ONT.LIG.significant_regions.fasta	DNA	1000

Background

Name	Freq.	Bg.				Bg.	Freq.	Name
Adenine	0.262	0.261	A	~	T	0.266	0.267	Thymine
Cytosine	0.232	0.232	C	~	G	0.240	0.240	Guanine

Other Settings

Motif Site Distribution	ZOOPS: Zero or one site per sequence
Site Strand Handling	Sites must be on the given strand
Maximum Number of Motifs	50
Motif E-value Threshold	no limit
Minimum Motif Width	8
Maximum Motif Width	50
Minimum Sites per Motif	2
Maximum Sites per Motif	1000
Show Advanced Settings	

MEME version
4.12.0 (Release date: Tue Jun 27 16:22:50 2017 -0700)

Reference
Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology*, pp. 28-36, AAAI Press, Menlo Park, California, 1994.

Command line
meme -oc UMIGS.ONT.LIG.meme -dna -mod zoops -nmotifs 50 UMIGS.ONT.LIG.significant_regions.fasta

